

RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.**

Application Serial Number: 10/555,060
Source: PCT/10
Date Processed by STIC: 11/8/05

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PCT

RAW SEQUENCE LISTING

DATE: 11/08/2005

PATENT APPLICATION: US/10/555,060

TIME: 12:21:53

Input Set : A:\065691-0413 Sequence Listing.txt

Output Set: N:\CRF4\11082005\J555060.raw

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3 <110> APPLICANT: AB Science
4     KINET Jean -Pierre
5     MOUSSY Alain
7 <120> TITLE OF INVENTION: Use of tyrosine kinase inhibitors for treating cerebral
ischemia
9 <130> FILE REFERENCE: D21220 NT
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/555,060
C--> 11 <141> CURRENT FILING DATE: 2005-10-28
11 <150> PRIOR APPLICATION NUMBER: US 60/465,789
12 <151> PRIOR FILING DATE: 2003-04-28
14 <160> NUMBER OF SEQ ID NOS: 5
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 976
20 <212> TYPE: PRT
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Human c-kit
26 <400> SEQUENCE: 1
27 Met Arg Gly Ala Arg Gly Ala Trp Asp Phe Leu Cys Val Leu Leu Leu
28   1           5           10           15
30 Leu Leu Arg Val Gln Thr Gly Ser Ser Gln Pro Ser Val Ser Pro Gly
31           20           25           30
33 Glu Pro Ser Pro Pro Ser Ile His Pro Gly Lys Ser Asp Leu Ile Val
34           35           40           45
36 Arg Val Gly Asp Glu Ile Arg Leu Leu Cys Thr Asp Pro Gly Phe Val
37           50           55           60
39 Lys Trp Thr Phe Glu Ile Leu Asp Glu Thr Asn Glu Asn Lys Gln Asn
40           65           70           75           80
42 Glu Trp Ile Thr Glu Lys Ala Glu Ala Thr Asn Thr Gly Lys Tyr Thr
43           85           90           95
45 Cys Thr Asn Lys His Gly Leu Ser Asn Ser Ile Tyr Val Phe Val Arg
46           100          105          110
48 Asp Pro Ala Lys Leu Phe Leu Val Asp Arg Ser Leu Tyr Gly Lys Glu
49           115          120          125
51 Asp Asn Asp Thr Leu Val Arg Cys Pro Leu Thr Asp Pro Glu Val Thr
52           130          135          140
54 Asn Tyr Ser Leu Lys Gly Cys Gln Gly Lys Pro Leu Pro Lys Asp Leu
55           145          150          155          160
57 Arg Phe Ile Pro Asp Pro Lys Ala Gly Ile Met Ile Lys Ser Val Lys
58           165          170          175
60 Arg Ala Tyr His Arg Leu Cys Leu His Cys Ser Val Asp Gln Glu Gly
61           180          185          190
63 Lys Ser Val Leu Ser Glu Lys Phe Ile Leu Lys Val Arg Pro Ala Phe

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64          195          200          205
66 Lys Ala Val Pro Val Val Ser Val Ser Lys Ala Ser Tyr Leu Leu Arg
67      210          215          220
69 Glu Gly Glu Glu Phe Thr Val Thr Cys Thr Ile Lys Asp Val Ser Ser
70 225          230          235          240
72 Ser Val Tyr Ser Thr Trp Lys Arg Glu Asn Ser Gln Thr Lys Leu Gln
73          245          250          255
75 Glu Lys Tyr Asn Ser Trp His His Gly Asp Phe Asn Tyr Glu Arg Gln
76          260          265          270
78 Ala Thr Leu Thr Ile Ser Ser Ala Arg Val Asn Asp Ser Gly Val Phe
79          275          280          285
81 Met Cys Tyr Ala Asn Asn Thr Phe Gly Ser Ala Asn Val Thr Thr Thr
82          290          295          300
84 Leu Glu Val Val Asp Lys Gly Phe Ile Asn Ile Phe Pro Met Ile Asn
85 305          310          315          320
87 Thr Thr Val Phe Val Asn Asp Gly Glu Asn Val Asp Leu Ile Val Glu
88          325          330          335
90 Tyr Glu Ala Phe Pro Lys Pro Glu His Gln Gln Trp Ile Tyr Met Asn
91          340          345          350
93 Arg Thr Phe Thr Asp Lys Trp Glu Asp Tyr Pro Lys Ser Glu Asn Glu
94          355          360          365
96 Ser Asn Ile Arg Tyr Val Ser Glu Leu His Leu Thr Arg Leu Lys Gly
97          370          375          380
99 Thr Glu Gly Gly Thr Tyr Thr Phe Leu Val Ser Asn Ser Asp Val Asn
100 385          390          395          400
102 Ala Ala Ile Ala Phe Asn Val Tyr Val Asn Thr Lys Pro Glu Ile Leu
103          405          410          415
105 Thr Tyr Asp Arg Leu Val Asn Gly Met Leu Gln Cys Val Ala Ala Gly
106          420          425          430
108 Phe Pro Glu Pro Thr Ile Asp Trp Tyr Phe Cys Pro Gly Thr Glu Gln
109          435          440          445
111 Arg Cys Ser Ala Ser Val Leu Pro Val Asp Val Gln Thr Leu Asn Ser
112          450          455          460
114 Ser Gly Pro Pro Phe Gly Lys Leu Val Val Gln Ser Ser Ile Asp Ser
115 465          470          475          480
117 Ser Ala Phe Lys His Asn Gly Thr Val Glu Cys Lys Ala Tyr Asn Asp
118          485          490          495
120 Val Gly Lys Thr Ser Ala Tyr Phe Asn Phe Ala Phe Lys Gly Asn Asn
121          500          505          510
123 Lys Glu Gln Ile His Pro His Thr Leu Phe Thr Pro Leu Leu Ile Gly
124          515          520          525
126 Phe Val Ile Val Ala Gly Met Met Cys Ile Ile Val Met Ile Leu Thr
127          530          535          540
129 Tyr Lys Tyr Leu Gln Lys Pro Met Tyr Glu Val Gln Trp Lys Val Val
130 545          550          555          560
132 Glu Glu Ile Asn Gly Asn Asn Tyr Val Tyr Ile Asp Pro Thr Gln Leu
133          565          570          575
135 Pro Tyr Asp His Lys Trp Glu Phe Pro Arg Asn Arg Leu Ser Phe Gly
136          580          585          590

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138 Lys Thr Leu Gly Ala Gly Ala Phe Gly Lys Val Val Glu Ala Thr Ala
139          595          600          605
141 Tyr Gly Leu Ile Lys Ser Asp Ala Ala Met Thr Val Ala Val Lys Met
142          610          615          620
144 Leu Lys Pro Ser Ala His Leu Thr Glu Arg Glu Ala Leu Met Ser Glu
145 625          630          635          640
147 Leu Lys Val Leu Ser Tyr Leu Gly Asn His Met Asn Ile Val Asn Leu
148          645          650          655
150 Leu Gly Ala Cys Thr Ile Gly Gly Pro Thr Leu Val Ile Thr Glu Tyr
151          660          665          670
153 Cys Cys Tyr Gly Asp Leu Leu Asn Phe Leu Arg Arg Lys Arg Asp Ser
154          675          680          685
156 Phe Ile Cys Ser Lys Gln Glu Asp His Ala Glu Ala Ala Leu Tyr Lys
157          690          695          700
159 Asn Leu Leu His Ser Lys Glu Ser Ser Cys Ser Asp Ser Thr Asn Glu
160 705          710          715          720
162 Tyr Met Asp Met Lys Pro Gly Val Ser Tyr Val Val Pro Thr Lys Ala
163          725          730          735
165 Asp Lys Arg Arg Ser Val Arg Ile Gly Ser Tyr Ile Glu Arg Asp Val
166          740          745          750
168 Thr Pro Ala Ile Met Glu Asp Asp Glu Leu Ala Leu Asp Leu Glu Asp
169          755          760          765
171 Leu Leu Ser Phe Ser Tyr Gln Val Ala Lys Gly Met Ala Phe Leu Ala
172          770          775          780
174 Ser Lys Asn Cys Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu
175 785          790          795          800
177 Thr His Gly Arg Ile Thr Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp
178          805          810          815
180 Ile Lys Asn Asp Ser Asn Tyr Val Val Lys Gly Asn Ala Arg Leu Pro
181          820          825          830
183 Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Cys Val Tyr Thr Phe
184          835          840          845
186 Glu Ser Asp Val Trp Ser Tyr Gly Ile Phe Leu Trp Glu Leu Phe Ser
187          850          855          860
189 Leu Gly Ser Ser Pro Tyr Pro Gly Met Pro Val Asp Ser Lys Phe Tyr
190 865          870          875          880
192 Lys Met Ile Lys Glu Gly Phe Arg Met Leu Ser Pro Glu His Ala Pro
193          885          890          895
195 Ala Glu Met Tyr Asp Ile Met Lys Thr Cys Trp Asp Ala Asp Pro Leu
196          900          905          910
198 Lys Arg Pro Thr Phe Lys Gln Ile Val Gln Leu Ile Glu Lys Gln Ile
199          915          920          925
201 Ser Glu Ser Thr Asn His Ile Tyr Ser Asn Leu Ala Asn Cys Ser Pro
202          930          935          940
204 Asn Arg Gln Lys Pro Val Val Asp His Ser Val Arg Ile Asn Ser Val
205 945          950          955          960
207 Gly Ser Thr Ala Ser Ser Ser Gln Pro Leu Leu Val His Asp Asp Val
208          965          970          975
214 <210> SEQ ID NO: 2

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215 <211> LENGTH: 30
216 <212> TYPE: DNA
217 <213> ORGANISM: Homo sapiens
219 <220> FEATURE:
220 <223> OTHER INFORMATION: Primer
222 <400> SEQUENCE: 2
223 aagaagagat ggtacctcga ggggtgaccc 30
226 <210> SEQ ID NO: 3
227 <211> LENGTH: 33
228 <212> TYPE: DNA
229 <213> ORGANISM: Homo sapiens
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Primer
234 <400> SEQUENCE: 3
235 ctgcttcgcg gccgcgttaa ctcttctcaa cca 33
238 <210> SEQ ID NO: 4
239 <211> LENGTH: 20
240 <212> TYPE: DNA
241 <213> ORGANISM: Homo sapiens
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Primer
246 <400> SEQUENCE: 4
247 agctcgttta gtgaaccgtc 20
250 <210> SEQ ID NO: 5
251 <211> LENGTH: 20
252 <212> TYPE: DNA
253 <213> ORGANISM: Homo sapiens
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Primer
258 <400> SEQUENCE: 5
259 gtcagacaaa atgatgcaac 20

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date